

(FILE 'HOME' ENTERED AT 11:53:16 ON 01 AUG 2003)

FILE 'REGISTRY' ENTERED AT 11:53:29 ON 01 AUG 2003

L1 2 S ACGCATAGGGCGCGAATTCCAAGGCGGCAGTAGTGAGGAT/SQSN
L2 2 S TCTTTGTCAAGGAAATGCAATGCAGCTTATAAAGTCAACA/SQSN
L3 3 S TGAGAGAGAACAGGAAGAAGATGAGGAAGAAGAATTTGGT/SQSN
L4 2 S MAALCEEEQVFLEPEB/SQSP
L5 0 S DGD LFDNGVGNEMDSN/SQSP
L6 2 S DGD LFDNGVENEMDSN/SQSP
L7 28 S GACGGCGGGAGCCGCTGCTCTCCGGCTGAGGGAATCAGAG/SQSN
L8 28 DUP REM L7 (0 DUPLICATES REMOVED)
L9 14 S AGAAAGAGGAGAGAAAAATGGAAAAAATTAGACAGCTAAA/SQSN
L10 9 S GCCGTGGGACCACTTTTTCCTACAGCAGGAGGATTTCAGATCTCCTTCC/SQSN
L11 580 S CTTTGGGAGGCCGAGGTGGGTGGATCACAAGGTCAGGAGA/SQSN
L12 5 S L7 AND L9 AND L10 AND L11
L13 3 S MTGEVGSEVHLEINDP/SQSP
L14 6 S TTDRKSSKKHIHDKEG/SQSP
L15 0 S KGTQIITGSDESCRKD/SQSP
L16 3 S L13 AND L14

FILE 'CAPLUS' ENTERED AT 12:18:44 ON 01 AUG 2003

L17 1 S 413634-54-5/RN
S 299147-70-9/REG#

FILE 'REGISTRY' ENTERED AT 12:20:09 ON 01 AUG 2003

L18 1 S 299147-70-9/RN

FILE 'CAPLUS' ENTERED AT 12:20:09 ON 01 AUG 2003

L19 2 S L18
S 413634-57-8/REG#

FILE 'REGISTRY' ENTERED AT 12:21:08 ON 01 AUG 2003

L20 1 S 413634-57-8/RN

FILE 'CAPLUS' ENTERED AT 12:21:09 ON 01 AUG 2003

L21 1 S L20
S 334026-68-5/REG#

FILE 'REGISTRY' ENTERED AT 12:21:27 ON 01 AUG 2003

L22 1 S 334026-68-5/RN

FILE 'CAPLUS' ENTERED AT 12:21:28 ON 01 AUG 2003

L23 1 S L22
S 438402-51-8/REG#

FILE 'REGISTRY' ENTERED AT 12:21:54 ON 01 AUG 2003

L24 1 S 438402-51-8/RN

FILE 'CAPLUS' ENTERED AT 12:21:54 ON 01 AUG 2003

L25 1 S L24
S 413634-58-9/REG#

FILE 'REGISTRY' ENTERED AT 12:23:02 ON 01 AUG 2003

L26 1 S 413634-58-9/RN

FILE 'CAPLUS' ENTERED AT 12:23:03 ON 01 AUG 2003

L27 1 S L26
S 413634-55-6/REG#

FILE 'REGISTRY' ENTERED AT 12:23:19 ON 01 AUG 2003

L28 1 S 413634-55-6/RN

FILE 'CAPLUS' ENTERED AT 12:23:19 ON 01 AUG 2003

L29 1 S L28

S 299147-69-6/REG#

L30 FILE 'REGISTRY' ENTERED AT 12:23:57 ON 01 AUG 2003
1 S 299147-69-6/RN

L31 FILE 'CAPLUS' ENTERED AT 12:23:57 ON 01 AUG 2003
2 S L30
S 264106-87-8/REG#

L32 FILE 'REGISTRY' ENTERED AT 12:24:23 ON 01 AUG 2003
1 S 264106-87-8/RN

L33 FILE 'CAPLUS' ENTERED AT 12:24:23 ON 01 AUG 2003
0 S L32
S 264106-87-8/REG#

L34 FILE 'REGISTRY' ENTERED AT 12:24:34 ON 01 AUG 2003
1 S 264106-87-8/RN

L35 FILE 'CAPLUS' ENTERED AT 12:24:34 ON 01 AUG 2003
0 S L34

L36 FILE 'GENBANK' ENTERED AT 12:24:49 ON 01 AUG 2003
1 S 264106-87-8

FILE 'CAPLUS' ENTERED AT 12:25:14 ON 01 AUG 2003
S 503249-20-5/REG#

L37 FILE 'REGISTRY' ENTERED AT 12:25:28 ON 01 AUG 2003
1 S 503249-20-5/RN

L38 FILE 'CAPLUS' ENTERED AT 12:25:29 ON 01 AUG 2003
1 S L37
S 413634-56-7/REG#

L39 FILE 'REGISTRY' ENTERED AT 12:26:04 ON 01 AUG 2003
1 S 413634-56-7/RN

L40 FILE 'CAPLUS' ENTERED AT 12:26:04 ON 01 AUG 2003
1 S L39
S 334026-67-4/REG#

L41 FILE 'REGISTRY' ENTERED AT 12:26:28 ON 01 AUG 2003
1 S 334026-67-4/RN


L42 FILE 'CAPLUS' ENTERED AT 12:26:28 ON 01 AUG 2003
1 S L41

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, CANCERLIT' ENTERED AT 12:26:59 ON
01 AUG 2003

L43 18 S CLASPIN

L44 5 DUP REM L43 (13 DUPLICATES REMOVED)

L Number	Hits	Search Text	DB	Time stamp
1	3	claspin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/01 12:29

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot		
Hosted by NCSC US	Mirror sites:	Bolivia	Canada	China	Switzerland	Taiwan

The Korean ExPASy site, kr.expasy.org, is temporarily not available.

Search for

NiceProt View of TrEMBL: Q9DF50

[Printer-friendly view](#)
[Quick BlastP search](#)

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the [user manual](#) or [other documents](#).

Entry information

Entry name	Q9DF50
Primary accession number	Q9DF50
Secondary accession numbers	None
Entered in TrEMBL in	Release 16, March 2001
Sequence was last modified in	Release 22, October 2002
Annotations were last modified in	Release 23, March 2003
Name and origin of the protein	
Protein name	Claspin
Synonyms	None
Gene name	None
From	<u>Xenopus laevis</u> (African clawed frog) [TaxID: 8355]
Taxonomy	<u>Eukaryota</u> ; <u>Metazoa</u> ; <u>Chordata</u> ; <u>Craniata</u> ; <u>Vertebrata</u> ; <u>Euteleostomi</u> ; <u>Amphibia</u> ; <u>Batrachia</u> ; <u>Anura</u> ; <u>Mesobatrachia</u> ; <u>Pipoidea</u> ; <u>Pipidae</u> ; <u>Xenopodinae</u> ; <u>Xenopus</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
MEDLINE=21000493; PubMed=11090622; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Kumagai A.](#), [Dunphy W.G.](#);
"Claspin, a novel protein required for the activation of Chk1 during a DNA replication checkpoint response in *Xenopus* egg extracts.";
Mol. Cell 6:839-849(2000).
- [2] SEQUENCE FROM NUCLEIC ACID.
[Kumagai A.](#), [Dunphy W.G.](#);
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	AF297867; AAG24516.2; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOVERGEN	[Family / Alignment / Tree]
ProtoMap	Q9DF50 .

PRESAGE Q9DF50.ModBase Q9DF50.SWISS-2DPAGE Get region on 2D PAGE.**Keywords**

None

Features

None

Sequence information

Length: **1285** Molecular weight: **145981** CRC64: **A302479768FDBA7D** [This is a checksum on the
AA Da sequence]

10	20	30	40	50	60
MAALCEEEQV	FLEPEDISLK	IVETDSDSGQ	GSCEMADQNK	LLGCVEDKDT	DDEILVRKKS
70	80	90	100	110	120
KKKEVLVDS	SDEELEMRF	ADNVKGHSN	EENEETMSAY	REKPRKIRSA	VLDSDNSDHE
130	140	150	160	170	180
LDVQISTSQN	AAEIPSEHD	SLEKETHTVK	PKTSKSLKKQ	TDTNKEEIVK	NKSKRKIPKE
190	200	210	220	230	240
KIKRRTKQKS	KAVAEARPNL	NDSGCLLTG	DLFDNGVENE	MDSNEEEDSL	EAIRAKMKSK
250	260	270	280	290	300
LNSHSAENFE	DFELDTGNQ	ESPEKRKERE	AARLGKEAMK	QMHSETQRLI	RESSVSLPYH
310	320	330	340	350	360
LPEPKTIHDF	FKRRPRPLCQ	GNAMQLIKST	KYQPCTEEKK	KPNEEICAIEV	PEFDYVSKED
370	380	390	400	410	420
LEISPEQPLL	NTQCSHAAYL	CVVQNDARTE	GLSKSTEAVV	TGQMNDHEDA	FSDSNIVHEQ
430	440	450	460	470	480
ETVGLITVTE	TFQTPFIPQP	ESVVCQIQN	DVVEMQRMPE	QPTHKPKLSK	LEKLKALGVD
490	500	510	520	530	540
LSIKPRLCPD	DGSFVNLEP	KPNKEFEALK	ERFLKHTLQK	SKPRTERKVN	LNIIRKETTA
550	560	570	580	590	600
DGKEELKADV	VPIVMATEKP	DKSIYQKPGE	KLQVLKVKLQ	EAMKIRRSEE	RLKRQALYKL
610	620	630	640	650	660
DNEDGFEDDE	EEEEEMTEESE	DDGDGNAETA	DYPGGEDEEE	VGDAEDDNDE	DDTVNDRLLG
670	680	690	700	710	720

```

NVPEIVIPLP RPVTTDSSLM LFKDNSSKLG DSLPDESGCK RSSRLEYEED SLLPQLKENS
      730      740      750      760      770      780
      |      |      |      |      |      |
HNSSFELISS MIPSYQPCNK TTRVVINSNN LGFRSPSPVH FKTSFLSSAS KSSGKMSEPS
      790      800      810      820      830      840
      |      |      |      |      |      |
LPVEDSQDLY NASPEPKASY LCAGRNSQFQ FSLEDDTQSQ LLDADGFLNV GRHKSSSAKH
      850      860      870      880      890      900
      |      |      |      |      |      |
RLALDTMDEN AMDANMDELL DLCSGQFKES LSGTSQAAES DAKKQPMDEL LELCSGKFVS
      910      920      930      940      950      960
      |      |      |      |      |      |
QADCSTQDSS ASAKDRSTAV KKDISDEVAT VSSSFLTERE QEEDEEEEFEG EFKLLPCDDS
      970      980      990      1000      1010      1020
      |      |      |      |      |      |
ESENEEQNEE EEEEEDAKDD EDEEEILQKQ QKRKLRLNDF MEDEAELSGS DVGSGDEYEG
      1030      1040      1050      1060      1070      1080
      |      |      |      |      |      |
DDDEYEEEA I DEDLPSDEEL QDQVNKIHMK VTMDDEDQRQL RFYQERYLAD GDLHSDGPGR
      1090      1100      1110      1120      1130      1140
      |      |      |      |      |      |
TRKFRWKHLD DASQVDMFRR DSELEEVDGE NEETEETELK WRKERFEREQ WLREQPQGSR
      1150      1160      1170      1180      1190      1200
      |      |      |      |      |      |
DNNEEEEEEDI GEDSQFMKLA KKVTAKALQR KVSTETNEPK KPGPRNPYEV IRPFSLPKLR
      1210      1220      1230      1240      1250      1260
      |      |      |      |      |      |
TGSLLSKPKE VLQKLA AVSD LNP NAPRNSR NEVFQTVSPG KKEETTDKPR SKVRKNIAVA
      1270      1280
      |      |
MPSPKRFKRD STPTVKRSR I FQ LLE

```

Q9DF50 in [FASTA](#)
format

[View entry in original TrEMBL format](#)

[View entry in raw text format \(no links\)](#)

[Request for annotation of this TrEMBL entry](#)

BLAST [BLAST submission on](#)
[ExPASy/SIB](#)
or at [NCBI \(USA\)](#)



Sequence analysis tools: [ProtParam](#), [ProtScale](#),
[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet](#) (Java)



[ScanProsite](#), [MotifScan](#)




Search the [SWISS-MODEL Repository](#)

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
--	--------------------------	-------------------------------	----------------------------	----------------------------

Hosted by NCSC US Mirror sites: Bolivia Canada China Switzerland Taiwan

The Korean ExPASy site, kr.expasy.org, is temporarily not available.

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
Hosted by NCSC US Mirror sites: Bolivia Canada China Switzerland Taiwan				

The Korean ExPASy site, kr.expasy.org, is temporarily not available.

Search for

NiceProt View of TrEMBL: Q9HAW4

[Printer-friendly view](#)
[Quick BlastP search](#)

[\[Entry info\]](#)
[\[Name and origin\]](#)
[\[References\]](#)
[\[Comments\]](#)
[\[Cross-references\]](#)
[\[Keywords\]](#)
[\[Features\]](#)
[\[Sequence\]](#)
[\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the [user manual](#) or [other documents](#).

Entry information

Entry name	Q9HAW4
Primary accession number	Q9HAW4
Secondary accession numbers	None
Entered in TrEMBL in	Release 16, March 2001
Sequence was last modified in	Release 16, March 2001
Annotations were last modified in	Release 25, September 2003
Name and origin of the protein	
Protein name	Hu-Claspin
Synonyms	None
Gene name	None
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota ; Metazoa ; Chordata ; Craniata ; Vertebrata ; Euteleostomi ; Mammalia ; Eutheria ; Primates ; Catarrhini ; Hominidae ; Homo .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 MEDLINE=21000493; PubMed=11090622; [NCBI, ExPASy, EBI, Israel, Japan]
[Kumagai A.](#), [Dunphy W.G.](#);
 "Claspin, a novel protein required for the activation of Chk1 during a DNA replication checkpoint response in *Xenopus* egg extracts."; [Mol. Cell](#) 6:839-849(2000).

Comments

None

Cross-references

EMBL	AF297866 ; AAG24515.1 ; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
Genew	HGNC:19715 ; CLSPN .
CleanEx	HGNC:19715 ; CLSPN .
GO	GO:0005515 ; Molecular function: protein binding (<i>non-traceable author statement</i>).
Ensembl	Q9HAW4 ; Homo sapiens . [Entry / Contig view]
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOVERGEN	[Family / Alignment / Tree]

ProtoMap Q9HAW4.PRESAGE Q9HAW4.ModBase Q9HAW4.SWISS-2DPAGE Get region on 2D PAGE.**Keywords**

None

Features

None

Sequence informationLength: **1332** Molecular weight:**AA 150175 Da**CRC64: **4EA38DC16A3936C3** [This is a checksum on the sequence]

10	20	30	40	50	60
MTGEVGSEVH	LEINDPNVIS	QEEADSPSDS	GQGSYETIGP	LSEGDSDEEI	FVSKKLKNRK
70	80	90	100	110	120
VLQDSDSETE	DTNASPEKTT	YDSAEENKE	NLYAGKNTKI	KRIYKTVADS	DESYMEKSLY
130	140	150	160	170	180
QENLEAQVKP	CLELSLQSGN	STDFTTDRKS	SKKHIHDKEG	TAGKAKVKSK	RRLEKEERKM
190	200	210	220	230	240
EKIRQLKKKE	TKNQEDDVEQ	PFNDSGCLLV	DKDLFETGLE	DENNSPLEDE	ESLESIRAAV
250	260	270	280	290	300
KNKVKKHKKK	EPSLESGVHS	FEEGSELSKG	TTRKERKAAR	LSKEALKQLH	SETQRLIRES
310	320	330	340	350	360
ALNLPYHMPE	NKTIHDFFR	KPRPTCHGNA	MALLKSSKYQ	SSHKKEIIDT	ANTTEMNSDH
370	380	390	400	410	420
HSKGSEQTTG	AENEVETNAL	PVVSKEIQII	TGSDSCRKD	LVKNEELEIQ	EKQKQSDIRP
430	440	450	460	470	480
SPGDSSVLQQ	ESNFLGNNHS	EECQVGLVA	FEPHALEGE	PQNPEETDEK	VEEPEQQNKS
490	500	510	520	530	540
SAVGPPEKVR	RFTLDRLKQL	GVDVSIKPR	GADEDSFVIL	EPETNRELEA	LKQRFWKHAN
550	560	570	580	590	600
PAAKPRAGQT	VNVNVIVKDM	GTDGKEELKA	DVVPVTLAPK	KLDGASHTKP	GEKLQVLKAK
610	620	630	640	650	660
LQEAMKLRRF	EERQKRQALF	KLDNEDGSEE	EEEEEEEMTD	ESEEDGEKVV	EKEEKEEELE
670	680	690	700	710	720

```

      |      |      |      |      |      |
EEEGKEEEEE EEGNQETAEF LLSSEEIETK DEKEMDKENN DGSSEIGKAV GFLSVPKSLS
      |      |      |      |      |      |
      730      740      750      760      770      780
      |      |      |      |      |      |
SDSTLLLFKD SSSKMGYSPT EEKSETDENS GKQPSKLEDE DSCSLLTKEK SHNSSFELIG
      |      |      |      |      |      |
      790      800      810      820      830      840
      |      |      |      |      |      |
STIPSYQPCN RQTGRGTSFF PTAGGFRSPS PGLFRASLVS SASKSSGKLS EPSLPIEDSQ
      |      |      |      |      |      |
      850      860      870      880      890      900
      |      |      |      |      |      |
DLYNASPEPK TLFLGAGDFQ FCLEDDTQSQ LLDADGFLNV RNHRNQYQAL KPRLPLASMD
      |      |      |      |      |      |
      910      920      930      940      950      960
      |      |      |      |      |      |
ENAMDANMDE LLDLCTGKFT SQA EKHLPRK SDKKENMEEL LNLCSGKFTS QDASTPASSE
      |      |      |      |      |      |
      970      980      990      1000      1010      1020
      |      |      |      |      |      |
LNKQEKESM GDPMEELAL CSGSFPTDKE EEEEEEEFGD FRLVSNDFEF DSDEDEHSDS
      |      |      |      |      |      |
     1030     1040     1050     1060     1070     1080
      |      |      |      |      |      |
GNDLALEDHE DDDEEELLKR SEKLKRQMRL RXYLEDEAEV SGSDVGSEDE YDGEEIDEYE
      |      |      |      |      |      |
     1090     1100     1110     1120     1130     1140
      |      |      |      |      |      |
EDVIDEVLPS DEELQSQIKK IHMKTMLDDD KRQLRLYQER YLADGDLHSD GPGRMRKFRW
      |      |      |      |      |      |
     1150     1160     1170     1180     1190     1200
      |      |      |      |      |      |
KNIDDASQMD LFHRSDDDQ TEEQLDESEA RWRKERIERE QWLRDMAQQG KITAEIIIIII
      |      |      |      |      |      |
     1210     1220     1230     1240     1250     1260
      |      |      |      |      |      |
GEDSQFMILA KKVTAALQK NASRPMVIQE SKSLLRNPFE AIRPGSAQQV KTGSLNQP
      |      |      |      |      |      |
     1270     1280     1290     1300     1310     1320
      |      |      |      |      |      |
AVLQKLAALS DHNPSAPRNS RNFVFHTLSP VKAEAAKES KSQKIPEKDS DWLTWSGAPI
      |
    1330
      |
PGFFRLSFDP HG

```

Q9HAW4 in
FASTA format

[View entry in original TrEMBL format](#)

[View entry in raw text format \(no links\)](#)


[Request for annotation of this TrEMBL entry](#)

BLAST [BLAST submission on](#)
[ExpASY/SIB](#)
or at [NCBI \(USA\)](#)



Sequence analysis tools: [ProtParam](#), [ProtScale](#),
[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet \(Java\)](#)

[ScanProsite](#), [MotifScan](#)Search the [SWISS-MODEL Repository](#)

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot		
Hosted by NCSC US	Mirror sites:	Bolivia	Canada	China	Switzerland	Taiwan

The Korean ExPASy site, kr.expasy.org, is temporarily not available.